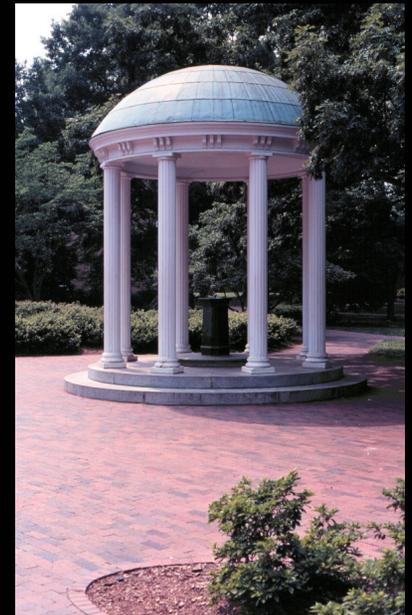


Molecular Epidemiology of BRAF and NRAS Mutations in Melanomas

**Nancy E. Thomas, MD PhD
Associate Professor
University of North Carolina
at Chapel Hill**



Questions

Do childhood and adult sun exposure increase melanoma risk?

Do common NER polymorphisms increase melanoma risk?

Are melanoma pathways (denoted by mutational status) differentially associated with sun exposure and moles?

Is there a mechanism by which BRAF mutations could arise related to sun exposure?

"GEM"

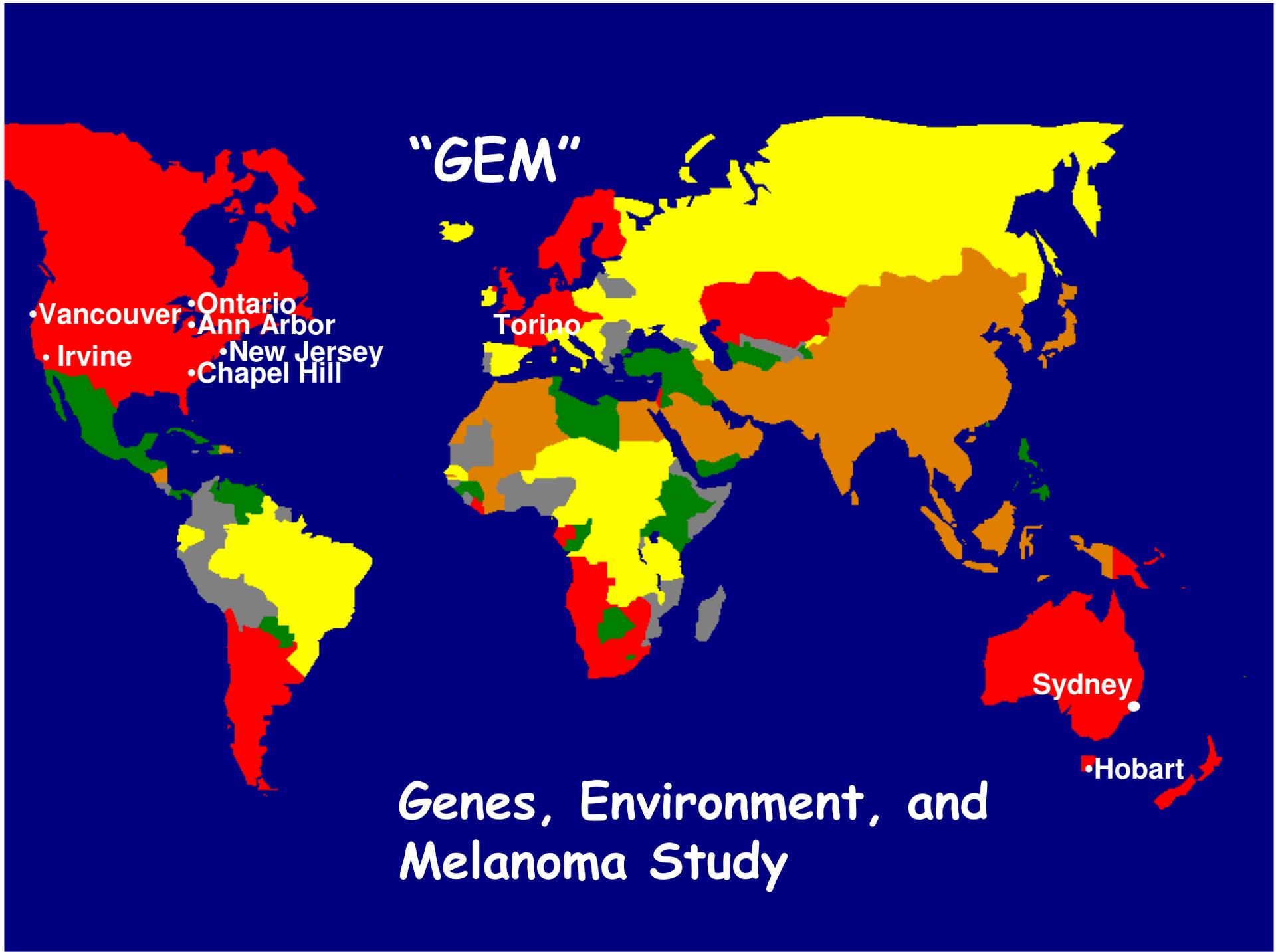
• Vancouver • Ontario
• Irvine • Ann Arbor
• New Jersey
• Chapel Hill

Torino

Sydney

• Hobart

Genes, Environment, and
Melanoma Study



GEM Study Design

Multiple Primary
“CASES”
n = 1238

Single Primary
“CONTROLS”
n = 2485

Sun exposure and phenotypic data

Inherited genetic markers
DNA repair polymorphisms

Somatic genetic markers
(tumor blocks)
BRAF, RAS

Interpretation of Results

Risk of second or higher order melanoma among persons with a first diagnosis of melanoma

approximates

Risk of first primary melanoma among persons who were previously unaffected

Begg. Int J Epidemiol, 2006

Sunlight Exposure in GEM

Ecologic level	Residence history linked to latitude, zenith angle, ozone column, surface elevation, cloud cover
Individual level	Recreational, occupational, vacations, sunburns

Strong Melanoma Risk Factors

Ecologic level	Childhood sun exposure by residence OR ~ 2
Individual level	Lifetime beach activities & holidays OR ~ 1.5

Kricker et al. Cancer Causes Control, 2006

DNA repair genes

Nucleotide excision repair gene
polymorphisms

XPD, HR23B, XPG, XPC, XPF, ERCC6

DNA repair genes

XPD 312 OR = 1.5 (1.2-1.9), P = 0.004

XPD 751 OR = 1.4 (1.1-1.7), P = 0.004

Strongest for diagnosis before age 30.

Number of *XPD 312 + 751* haplotypes:
trend P = 0.002

Millikan et al. Carcinogenesis 2006

DNA repair genes

Increased risk with increasing number of variant alleles for all NER genes combined:

trend $P = 0.02$

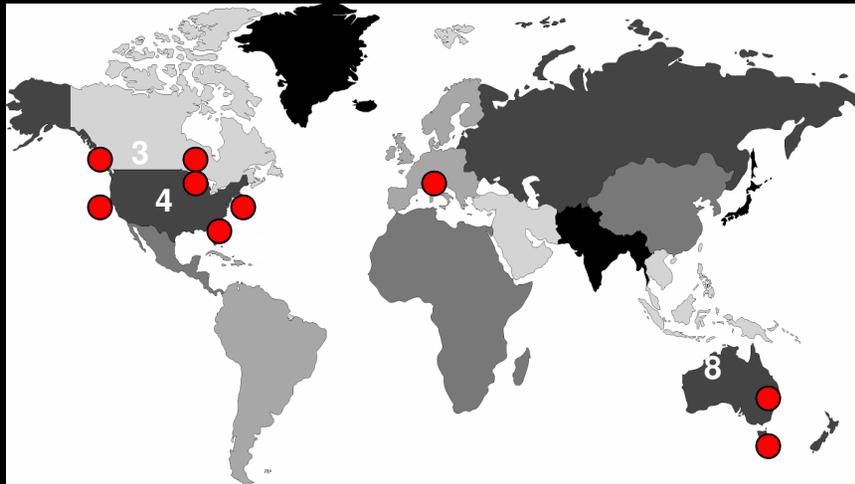
GEM Results

Somatic genetic markers

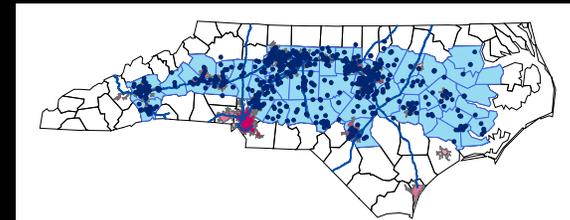
(tumor blocks)

BRAF, RAS

Nested GEM Study



214 cases in North Carolina, 2000



NC Cases (N=214)

Mean 51.8 years; 55% male

55.5% thin (< 0.75 mm)

79.7% SSM, 4.5% NM, 10.4% LMM, 5.5% other

Mutually Exclusive

BRAF+

NRAS-

BRAF-

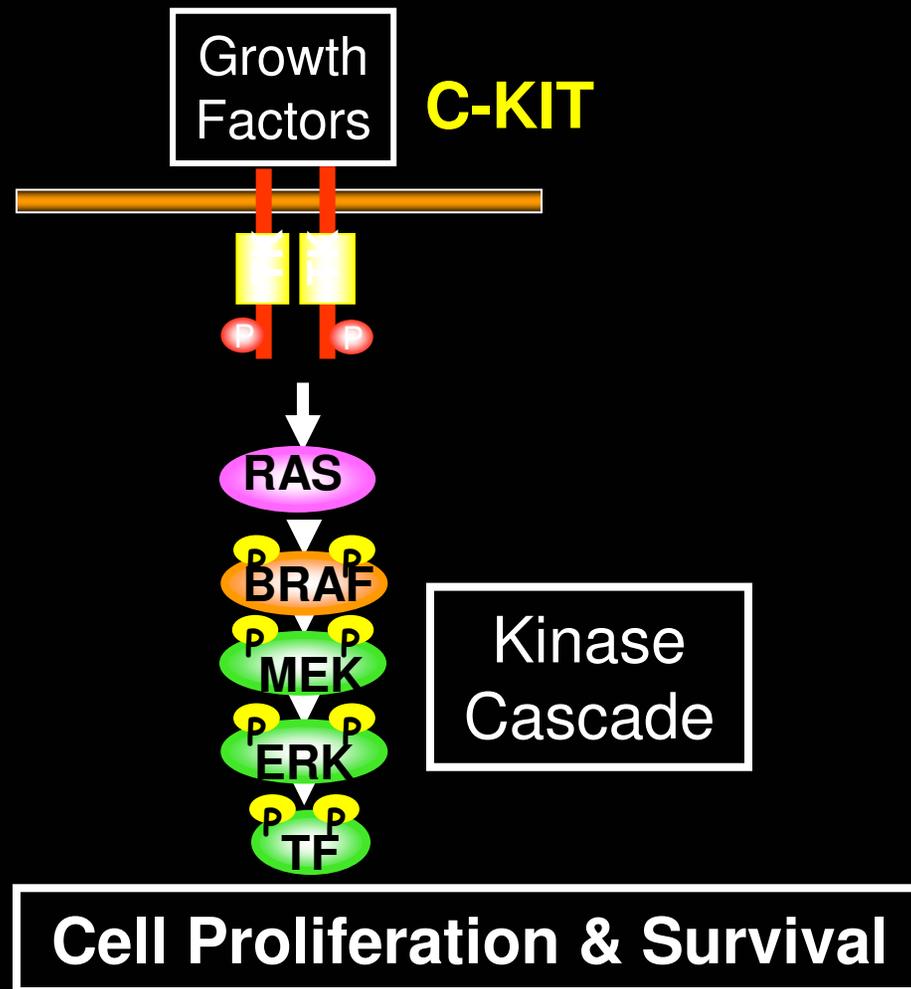
NRAS+

BRAF-

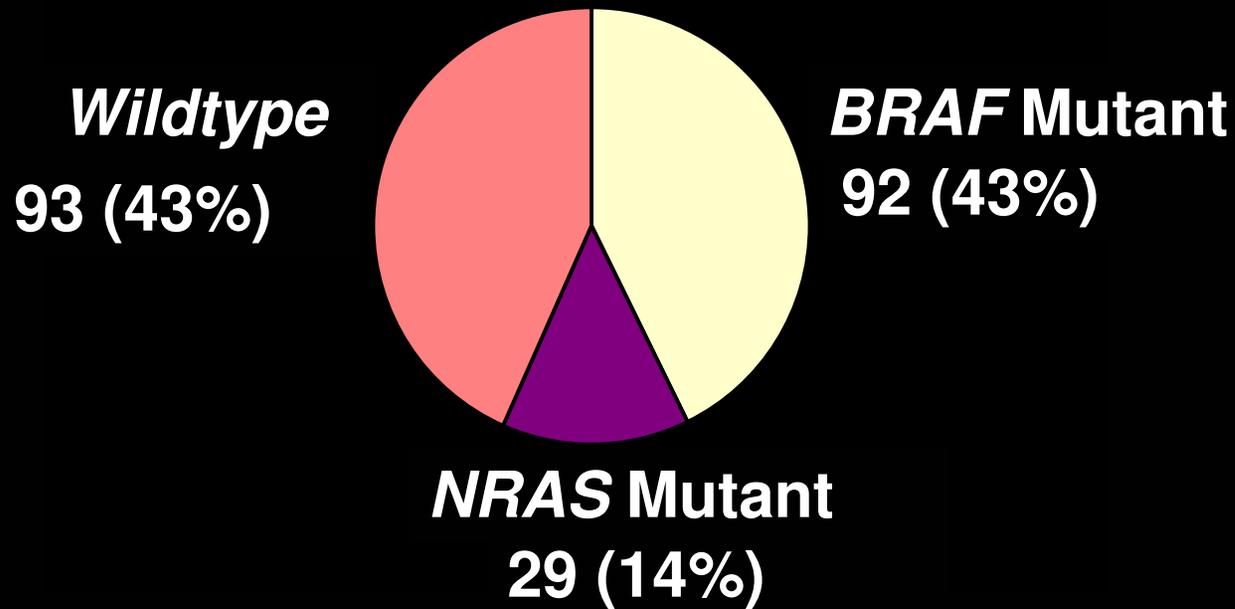
NRAS-

(wildtype)

MAPK Kinase Pathway Activation



Prevalence

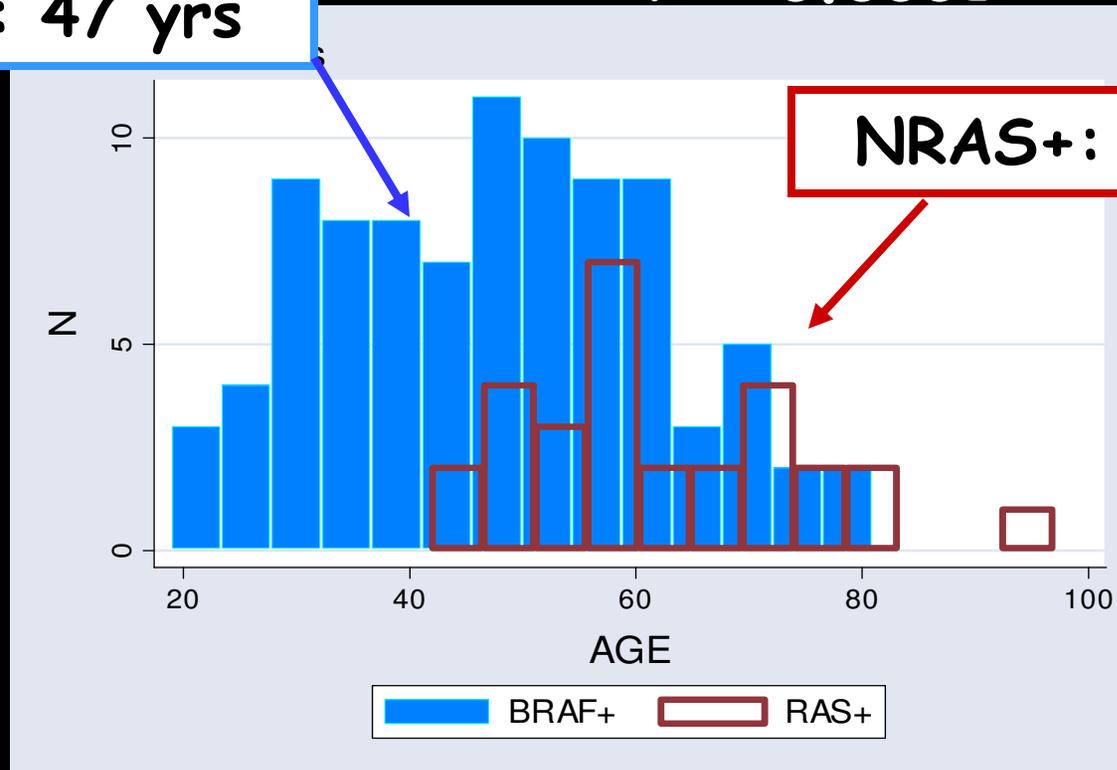


NRAS+ Decade older than BRAF+

BRAF+: 47 yrs

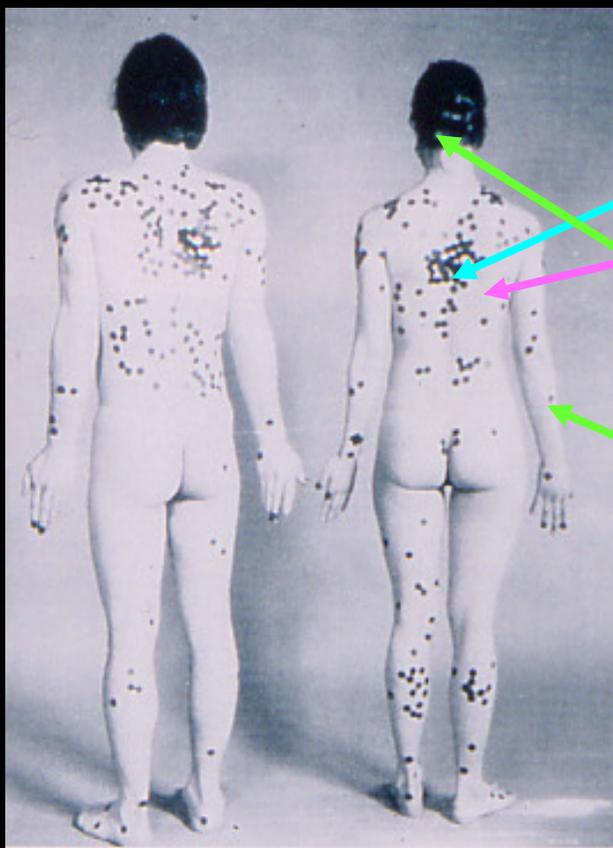
$P < 0.0001$

NRAS+: 62 yrs



Thomas et al., CEBP 2007

Anatomic Site



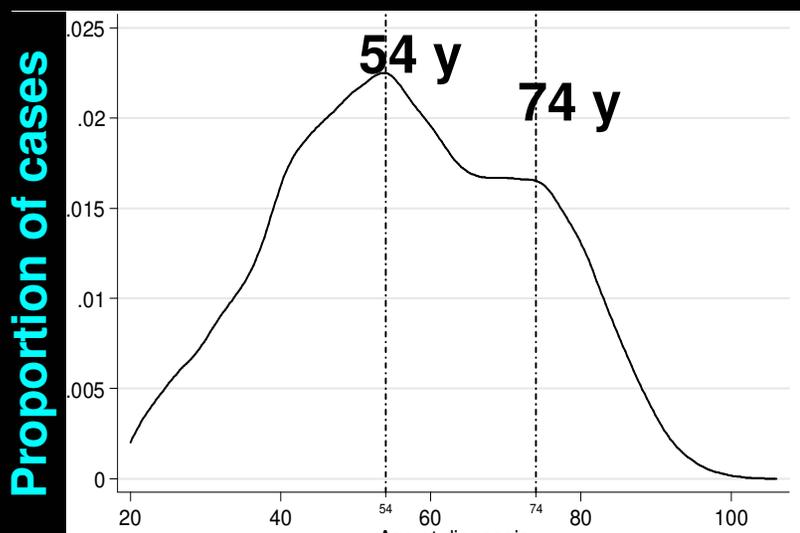
BRAF+

NRAS+

BRAF-
NRAS-
(wildtype)

Thomas et al. Cancer Epidemiol Biomarkers Prev 2007

Similar Evidence in SEER



Age at diagnosis

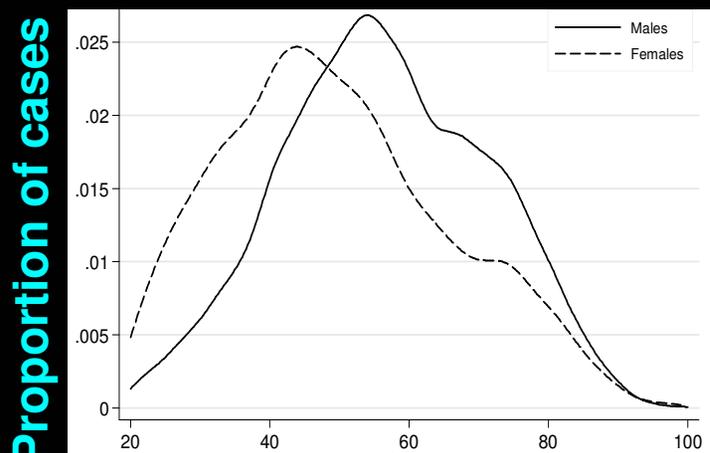
Age-density distribution

2000-2004

(n=48,673)

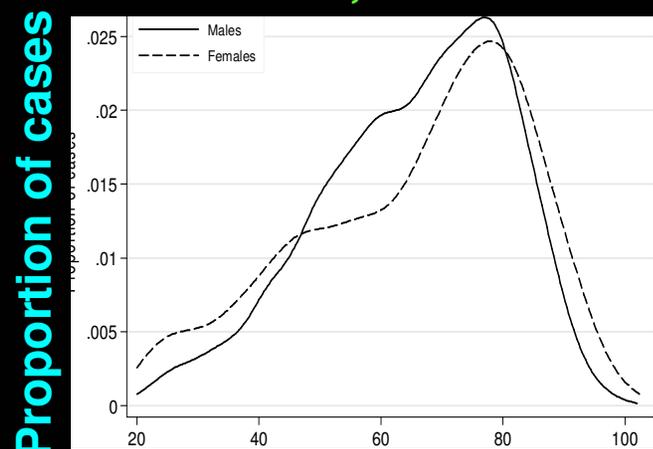
Lachiewicz et al.
JID 2007

Trunk



Age at diagnosis

Face, ears



Age at diagnosis

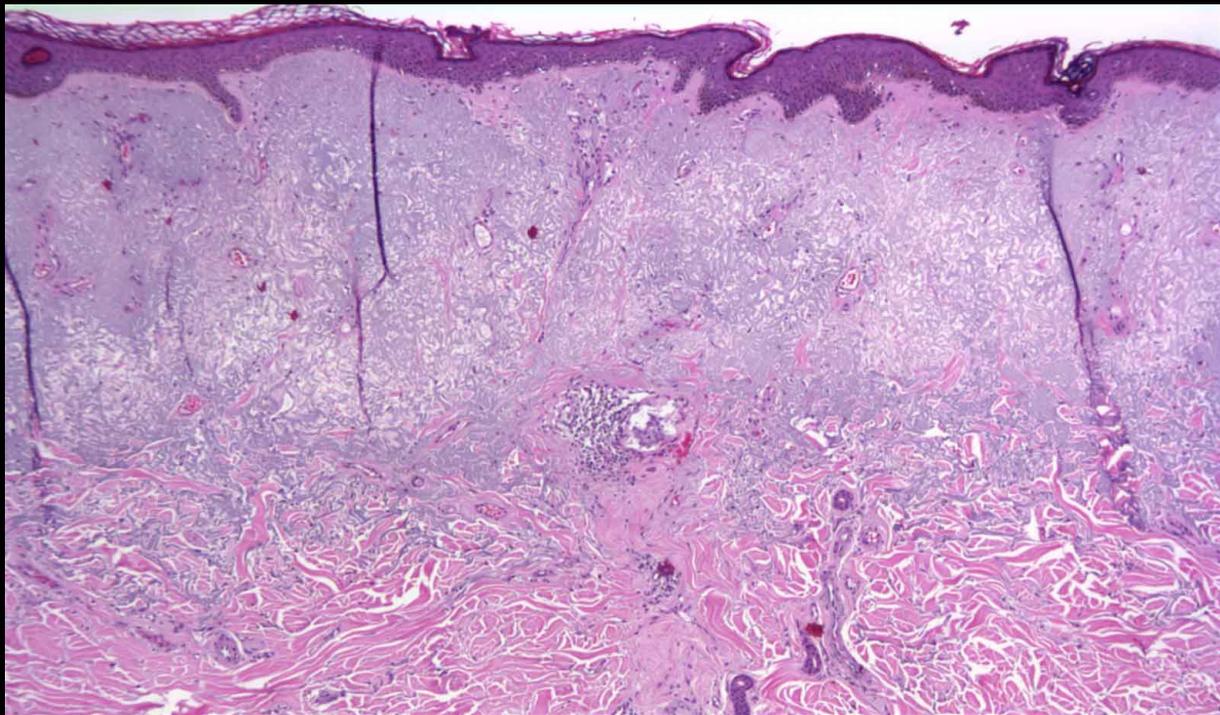
North Carolina GEM Cases

Tumor characteristics

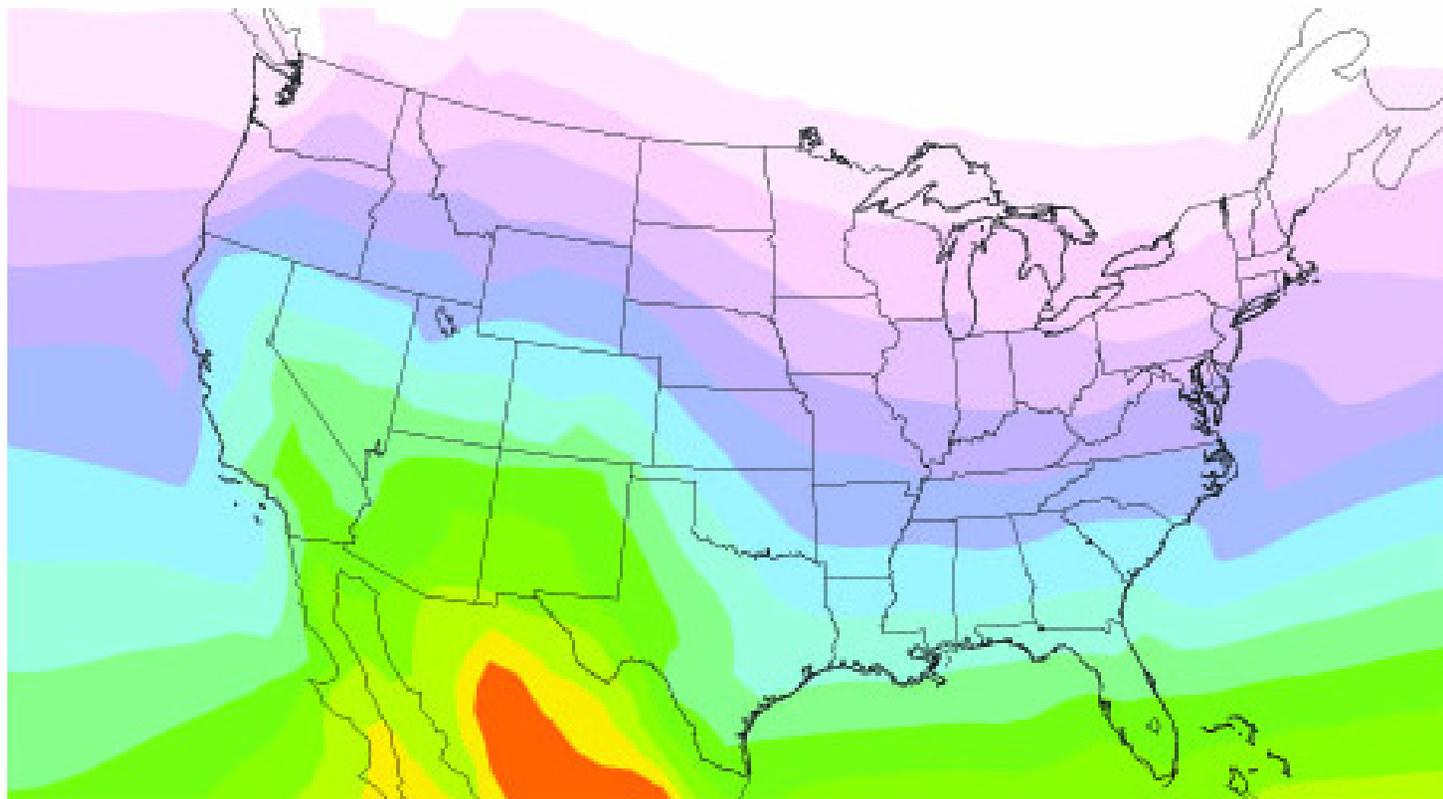
BRAF +	<ul style="list-style-type: none">• SSM, NM• Low solar elastosis
NRAS +	<ul style="list-style-type: none">• SSM, NM
BRAF – RAS –	<ul style="list-style-type: none">• LMM• High solar elastosis

Histologic Evidence of Solar Elastosis

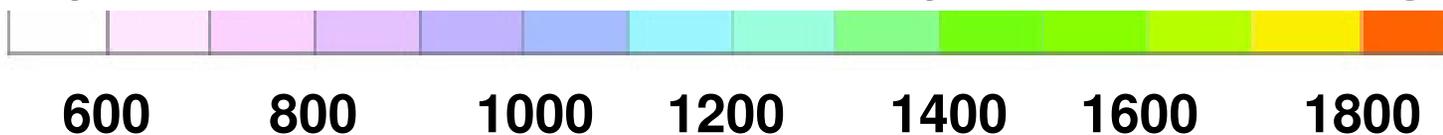
Homogenization of the superficial dermis



Erythemal UV Irradiance



Erythemal UV (250-400) KJ/m²/yr 1979-2000 avg.



Ambient Erythemal UV Exposure

Ambient Annual UV	<i>BRAF</i> ⁺ vs WT Age-adj OR (95% CI)	<i>NRAS</i> ⁺ vs WT Age-adj OR (95% CI)
Lifetime		
Low UV	1.0	1.0
High UV	2.0 (1.0-4.0)	1.1 (0.4-2.7)
Early life		
Low UV	1.0	1.0
High UV	2.6 (1.2-5.3)	0.9 (0.4-2.2)

Thomas et al. Cancer Epidemiol Biomarkers Prev 2007

Age of Ambient Erythemal UV Exposure

High UV irradiance	<i>BRAF</i> ₊ vs Wt Age-adj OR (95% CI)	<i>NRAS</i> ₊ vs WT Age-adj OR (95% CI)
Birth year	2.0 (1.0-4.1)	0.9 (0.4-2.2)
Age 10	1.9 (1.0-3.9)	0.8 (0.3-1.9)
Age 20	2.7 (1.3-5.7)	0.8 (0.3-1.9)
Age 30	1.0 (0.5-1.9)	0.7 (0.3-1.8)
Age 40	1.4 (0.6-3.3)	1.3 (0.5-3.4)
Age 50	1.2 (0.4-3.8)	2.5 (0.7-8.5)
Age 60	1.1 (0.2-7.0)	2.0 (0.4-9.8)

***BRAF* and *NRAS* Mutations in Moles**



- About 70% of moles have *BRAF* mutations
- Some moles have *NRAS* mutations
- Great majority of moles do not progress to melanoma

Pollock Nat Genet 2002; Kumar JID 2003; Yazdi JID 2003

Associations with Moles

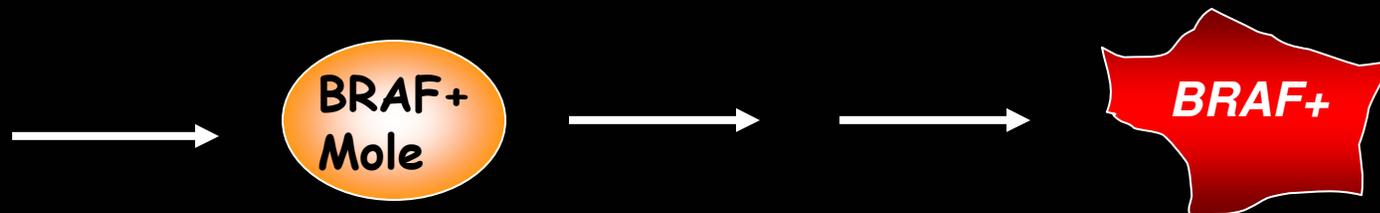
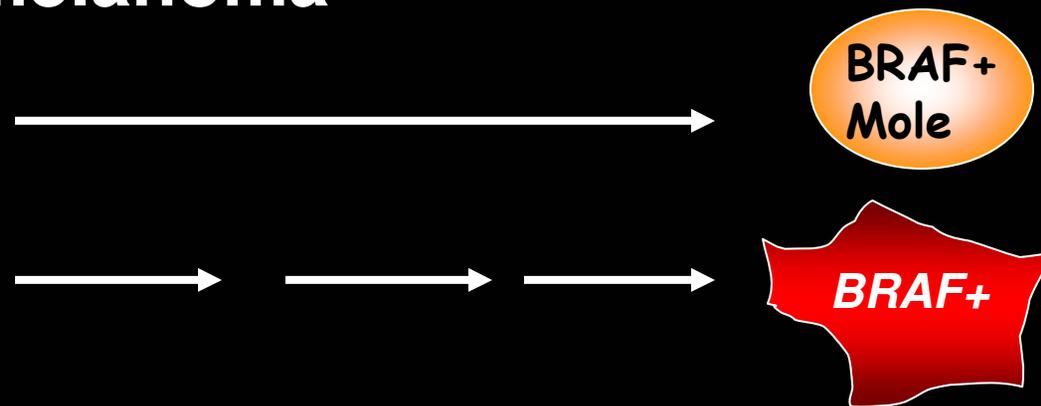
Characteristic	<i>BRAF</i> + vs WT Age-adj OR (95% CI)	<i>NRAS</i> + vs WT Age-adj OR (95% CI)
Back mole counts		
0-4	1.0	1.0
5-14	2.4 (1.1-5.5)	1.2 (0.4-3.7)
> 14	3.2 (1.4-7.0)	1.7 (0.6-4.8)
<i>P</i> _{trend}	0.006	0.34
Mole density diagrams		
None	1.0	1.0
Low	2.3 (1.0-5.2)	2.7 (0.8-8.6)
Medium to high	3.8 (1.4-10.4)	3.3 (0.7-14.9)
<i>P</i> _{trend}	0.009	0.10

Multivariate Model

Characteristic	<i>BRAF</i> ⁺ vs Wt	<i>NRAS</i> ⁺ vs Wt
	Age-adj OR (95% CI)	Age-adj OR (95% CI)
Age at diagnosis (per 10 yrs)	0.8 (0.7-1.0)	1.4 (1.1-1.9)
Back mole counts		
0-4	1.0	1.0
5-14	2.8 (1.2-6.4)	1.1 (0.4-3.3)
> 14	3.4 (1.5-7.8)	1.9 (0.6-5.5)
P_{trend}	0.004	0.27
Early life UV		
Low UV	1.0	1.0
High UV	2.6 (1.2-5.6)	0.9 (0.4-2.2)

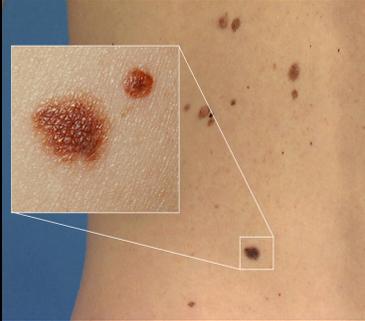
Are Moles Causal Intermediates for Some *BRAF*⁺ Melanomas?

- Mole-prone individuals are more likely to have *BRAF*⁺ melanoma



- Presence of a contiguous mole was associated with *BRAF*⁺ melanomas

Melanoma Models



**Mole
Prone**



**Mole
Resistant**

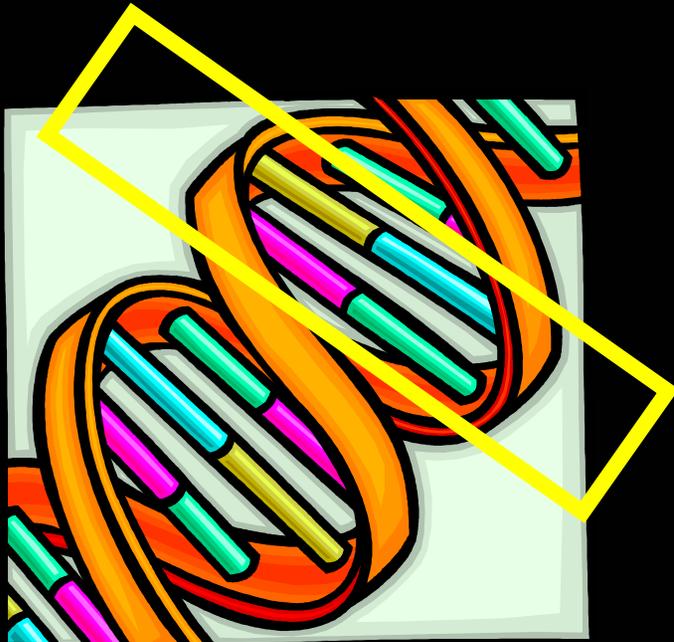
Habitual Sun?



↑ AGE

Tandem BRAF Mutations

10% of melanomas; rare in other BRAF-mutant tumors



Tissue-specific UV exposure?

Proposed mechanism:

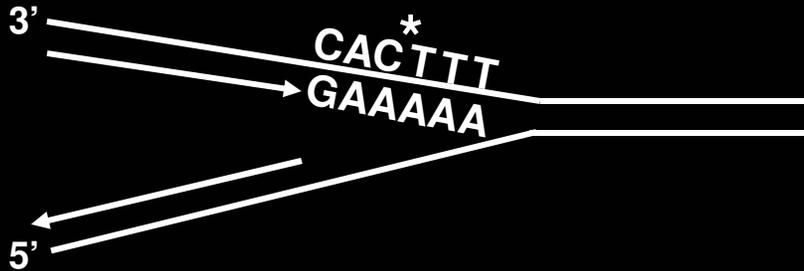
Nearby potential pyrimidine dimer sites

Specialized DNA polymerases

BRAF Mutations in Melanomas

Wild-type: 3' CGATGAC^{***}ACTTTAGA
 5' GCTACAG^{*}TGAAATCT^{**}

* Di-pyrimidines, potential sites for photoproduct formation



Mutagenic bypass of UVB-induced DNA lesions?

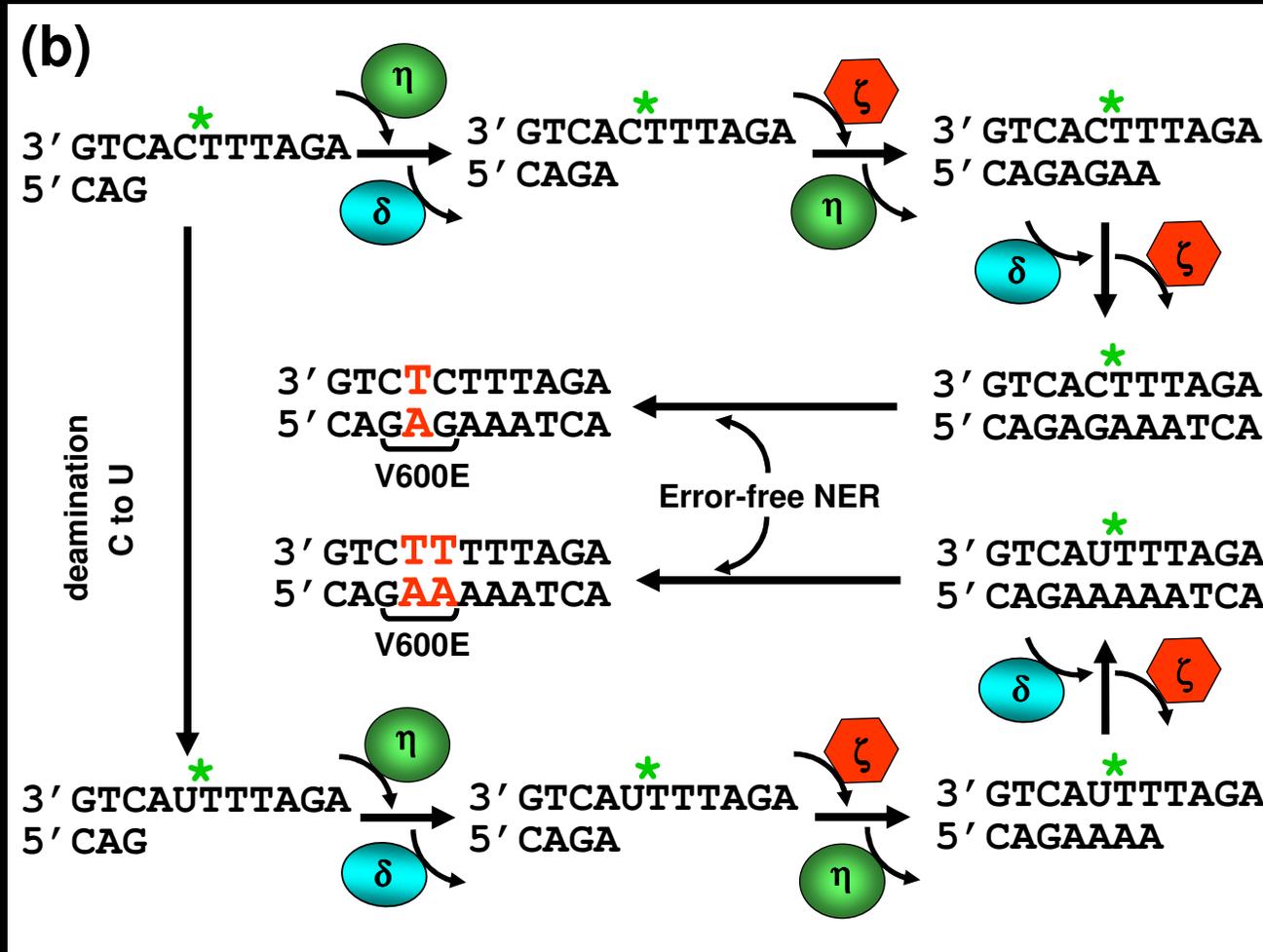
3' CGATGAC^TCCTTTAGA
 5' GCTACAG^AGAAATCT

t1799a Mutant

3' CGATGAC^{TT}TTTAGA
 5' GCTACAG^{AA}AAAATCT

tg1799aa Tandem Mutant

Inaccurate Polymerization?



Thomas NE, Berwick M, Cordeiro-Stone M, JID 2006

Answers

Childhood & adult sun exposure increase melanoma risk

Common NER polymorphisms increase melanoma risk

> OR with high waterside sun exposure

Melanomas pathways are differentially associated with sun exposure, modified by nevus propensity

BRAF mutations could arise from a mechanism involving nearby potential pyrimidine dimer sites, specialized DNA polymerases, and powerful selection

Future Plans

7 GEM sites participating in somatic tumor BRAF NRAS analysis

~1000 cases for analysis of risk and outcome

Relationship of XPD polymorphisms with NRAS and BRAF somatic mutations is being examined

Collaborators

UNC-GEM Melanoma Group

Robert Millikan
Kathleen Conway
Pam Groben
David Olilla
Bill Kaufmann
Marila Cordeiro-Stone
Norman Sharpless
Sharon N. Edmiston
Audrey Alexander
Honglin Hao
Anne Lachiewicz
Dianne Mattingly
Jessica Tse
Janiel Shields

GEM Melanoma Group

Marianne Berwick
Colin Begg
Klaus Busam
Bruce Armstrong

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